

DNA methylation and differentiation in plants

RINO CELLA * and GUIDO PEDRALI-NOY **

*Dipartimento di Genetica e Microbiologia, Università di Pavia, Via Abbiategrosso 207, 27100 Pavia - Italy; **Istituto di Genetica Biochimica ed Evoluzionistica del CNR, Via Abbiategrosso 207, 27100 Pavia - Italy.

ABSTRACT. – DNA methylation in plants appears to be a phenomenon more complex than in animals both for site specificity and the possible occurrence of two types of DNA methyltransferases. As in animals, DNA methylation appears to play a role in plant gene expression and differentiation (though recently acquired evidence indicated a less immediate relationship); other suggested roles for DNA methylation include genomic imprinting, paramutation and, to some extent, the gene silencing phenomenon observed in transgenic plants. However, while results obtained in mouse strictly link the presence of an active DNA methyltransferase with normal embryogenesis, in plants only circumstantial evidence points to the involvement of this enzyme in carrot somatic embryogenesis. What appears puzzling is the observation that hypomethylating mutants of *Arabidopsis thaliana* show normal development and morphology. The involvement of DNA methylation in plastid development is also debated. Of some interest appears the occurrence in plant cells of inhibitors of DNA methyltransferase activity although their biological significance and chemical nature remain to be elucidated.

Key words: asymmetric DNA methylation, DNA methyltransferase; embryogenesis, demethylation, *de novo* methylation, maintenance methylation, methylation inhibitors, symmetric DNA methylation.

INTRODUCTION

DNA of higher eukaryotes is almost generally characterised by the presence of a high content of the modified base 5-methylcytosine (5-MedC) which can account for up to 30% of total cytosines. While in animals methylation appears to occur mainly at CpG sites, in plants 5-MedC are found more frequently at CpNpG trinucleotides (GRUEMBAUM *et al.*, 1981; VANYUSHIN *et al.*, 1984). Despite its high methylation level, also plant DNA possesses unmethylated CpG islands (ANTEQUERA and BIRD, 1988); moreover, level and pattern of DNA methylation vary depending on tissues. For instance, in tomato, the level of methylation of mature tissues is significantly higher than that of immature ones and protoplasts (MESSENGER *et al.*, 1991) and in carrot, a different content of 5-MedC was observed among different tissues (PALMGREN *et al.*, 1991).

Lack of methylation in yeasts, *Drosophila* and *Caenorhabditis* has been interpreted by some authors as an indication of irrelevance of this DNA modification. However, since DNA methylation is mutagenic (deamination of 5-MedC causes the transition to thymine), its retention during evolution could be considered as an indication that it may serve a useful purpose (BIRD, 1992).